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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:21:15 ; Search time 11.88 seconds

(without alignments)
355.255 Million cell updates/sec

Title: US-09-754-826-2
Perfect score: 628
Sequence: 1 DEGLDCEHSTESRCRCRYPL.....KEQIYKIPAMVDRGCS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	99.0	375	1	GDF8_CHICK
2	622	99.0	375	1	GDF8_HUMAN
3	622	99.0	375	1	GDF8_MELGA
4	622	99.0	375	1	GDF8_PIG
5	622	99.0	376	1	GDF8_MOUSE
6	622	99.0	376	1	GDF8_MOUSE
7	616	98.1	375	1	GDF8_RAT
8	612	97.5	375	1	GDF8_PAPHA
9	611	97.3	375	1	GDF8_SHEEP
10	574	91.4	405	1	GDF8_BOVIN
11	574	91.4	405	1	GDF8_MOUSE
12	563	89.6	374	1	GDF8_HUMAN
13	527	83.9	345	1	GDF8_BRARE
14	241	38.4	235	1	GDF8_RAT
15	239	38.1	355	1	IHBB_MOUSE
16	236	37.6	391	1	DVRL_BRARE
17	235	37.4	349	1	IHBB_CHICK
18	235	37.4	407	1	IHBB_PIG
19	235	37.4	408	1	IHBB_HUMAN
20	225.5	35.9	207	1	IHBB_BOVIN
21	225.5	35.9	513	1	BMP6_RAT
22	223.5	35.6	510	1	BMP6_HUMAN
23	216.5	34.5	426	1	IHBA_MOUSE
24	212.5	33.8	360	1	IHBA_HORSE
25	211.5	33.7	125	1	DVRL_XENLA
26	211.5	33.7	352	1	GDF6_MOUSE
27	211.5	33.7	436	1	IHBC_MOUSE
28	210.5	33.5	424	1	GDF6_BOVIN
29	210.5	33.5	424	1	IHBA_MOUSE
30	210.5	33.5	424	1	IHBA_PIG
31	210.5	33.5	425	1	IHBA_RAT
32	210.5	33.5	425	1	IHBA_BOVIN
33	210.5	33.5	426	1	IHBA_SHEEP
					BMP7_XENLA

34	210.5	33.5	426	1	IHBA_HUMAN	P08476	homo sapien
35	209.5	33.4	431	1	BMP7_HUMAN	P18075	homo sapien
36	208.5	33.2	352	1	IHBC_HUMAN	P55103	homo sapien
37	207.5	33.0	151	1	GDF7_MOUSE	P43029	mus sapien
38	207.5	33.0	430	1	BMP7_MOUSE	P23359	mus sapien
39	206.5	32.9	495	1	GDF5_MOUSE	P43027	mus sapien
40	206.5	32.9	501	1	GDF5_HUMAN	P34820	homo sapien
41	205.5	32.7	350	1	BMP8_HUMAN	P08717	mus sapien
42	204.5	32.6	350	1	IHBE_MOUSE	O08959	rattus norv
43	204.5	32.6	350	1	IHBE_RAT	O9WUK5	rattus norv
44	204.5	32.6	351	1	IHBC_RAT	P92172	caenorhabdi
45	204	32.5	350	1	DAF7_CAEEL		

ALIGNMENTS

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RESULT 1
ID      GDF8_CHICK      STANDARD:      PRT:      375 AA.
AC      0A2220;
DT      15-JUL-1999 (Rel. 38, Created)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN      GDF8 OR MSTN.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=WHITE LEGHORN; TISSUE=Skeletal muscle;
RX      MEDLINE=98024153; PubMed=9356471;
RA      McPherron A.C., Lee S.-J.;
RT      "Double muscling in cattle due to mutations in the myostatin gene.";
RL      Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC      -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC      MUSCLE GROWTH.
CC      -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC      -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF019621; AAB86688.1; -
DR      HSSP: P18075; BMP.
DR      InterPro: IPR001839; TGF-beta.
DR      InterPro: IPR001111; TGFb.N.
DR      Pfam: PF00019; TGF-beta. 1.
DR      Pfam: PF00688; TGF-beta. 1.
DR      ProDom: PD000357; TGF-beta. 1.
DR      SMART: SM00204; TGFb. 1.
DR      PROSITE: PS00250; TGF-BETA_1; 1.
KW      Growth factor; Cytokine; Glycoprotein; Signal.
FT      SIGNAL      1      23
FT      PROPEP      24      266
FT      CHAIN      267      375
FT      DISULFID      281      340
FT      DISULFID      309      372
FT      DISULFID      313      374
FT      DISULFID      339      339
FT      CARBOHYD      71      71
SO      SEQUENCE      375 AA; 42707 MW; DA732DB9426E4DAF CRC64;

```

Query Match

99.0%; Score 622; DB 1; Length 375;

Best Local Similarity 99.1%; Pred. No. 4e-63;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDEHSTESRCRRPLTVDFEAFGMDWIAPRKRYKANCSCGCEFFVLOKYPHTL 60
|||||
DB 267 DFGDDEHSTESRCRRPLTVDFEAFGMDWIAPRKRYKANCSCGCEFFVLOKYPHTL 326
|||||

QY 61 VHOANPRGSAGPCCTPTLMSPINMLYFNKGEQIITYKIPAMVYDRGCS 109
|||||
DB 327 VHOANPRGSAGPCCTPTLMSPINMLYFNKGEQIITYKIPAMVYDRGCS 375
|||||

RESULT 2
ID GDF8_HUMAN STANDARD; PRT; 375 AA.
AC 014793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RC MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Muscle;
RC MEDLINE=99061972; PubMed=9843994;
RA Gonzalez-Cadavid N.F., Taylor W.E., Varsheski K., Sinha-Hikim I.,
Ma K., Ezzat S., Shen R., Lalani R., Asa S., Mamula M., Nair G.,
Arver S., Bhasin S.;
"Organization of the human myostatin gene and expression in healthy
men and HIV-infected men with muscle wasting.";
Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943(1998).
[3]
RN FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL: AF019627; AAB86694.1; -;
DR EMBL: AF104922; AAC96327.1; -;
DR HSSP: P18075; IBMP.
DR MIM: 601788; -;
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 26
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 313 374
BY SIMILARITY.

FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 42750 MW; EBF6129725E6AFA CRC64;

Query Match 99.0%; Score 622; DB 1; Length 375;
Best Local Similarity 99.1%; Pred. No. 4e-63;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDEHSTESRCRRPLTVDFEAFGMDWIAPRKRYKANCSCGCEFFVLOKYPHTL 60
|||||
DB 267 DFGDDEHSTESRCRRPLTVDFEAFGMDWIAPRKRYKANCSCGCEFFVLOKYPHTL 326
|||||

QY 61 VHOANPRGSAGPCCTPTLMSPINMLYFNKGEQIITYKIPAMVYDRGCS 109
|||||
DB 327 VHOANPRGSAGPCCTPTLMSPINMLYFNKGEQIITYKIPAMVYDRGCS 375
|||||

RESULT 3
ID GDF8_MELGA STANDARD; PRT; 375 AA.
AC 042221;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagrids.
NCBI_TaxID=9103;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RC MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
[2]
RN FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL: AF019625; AAB86692.1; ALF_INIT.
DR HSSP: P18075; IBMP.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 26
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 71 71
SQ SEQUENCE 375 AA; 42784 MW; D2AEAB732AEBA4E77 CRC64;

Query Match

99.0%; Score 622; DB 1; Length 375;

FT PROPER , 25 267 POTENTIAL.

FT	DISULFID	313	374	BY SIMILARITY.
FT	DISULFID	339	339	INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 375 AA; 42688 MW; 7B49B90ACAB926EA CRC64;

Query Match 98.1%; Score 616; DB 1; Length 375;
Best Local Similarity 98.2%; Pred. No. 1,9e-62;
Matches 107; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 60
DB 267 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 326

QY 61 VHOANPRGSAGPCTPTLMSPINMLYNGKKEQIIYGRKIPAMVYDRGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYNGKKEQIIYGRKIPAMVYDRGCS 375

RESULT 8
ID GDF8_SHEEP STANDARD; PRT; 375 AA.

AC 018830; 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.

OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;

RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;

RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.

CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: AF019622; AAB86689.1; -
CC HSSP: P12643; 3BMP.

DR Interpro: IPR001839; TGF-beta.
DR Interpro: IPR001111; TGF-beta_N.

DR Pfam: PF00619; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR Prodom: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.

KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.

FT PROPEP 24 266 POTENTIAL.

FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.

FT DISULFID 281 340 BY SIMILARITY.

FT DISULFID 309 372 BY SIMILARITY.

FT DISULFID 313 374 BY SIMILARITY.

FT CARBOHYD 48 48 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 375 AA; 42827 MW; 1C36F383BB11241 CRC64;

Query Match 97.5%; Score 612; DB 1; Length 375;
Best Local Similarity 96.3%; Pred. No. 5.5e-62;
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 60
DB 267 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 326

QY 61 VHOANPRGSAGPCTPTLMSPINMLYNGKKEQIIYGRKIPAMVYDRGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYNGKKEQIIYGRKIPAMVYDRGCS 375

RESULT 9
ID GDF8_BOVIN STANDARD; PRT; 375 AA.

AC 018836; 018829; 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN OR MH.

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RP SEQUENCE FROM N.A., AND VARIANT MH TYR-313.
RC STRAIN-FRIESIAN; TISSUE-Muscle, and Embryo;
RX MEDLINE=97458167; PubMed=9314496;

RA Kamadur R., Sharma M., Smith T.P.L., Bass J.J.;
RT "Mutations in myostatin (GDF8) in double-muscled Belgian Blue and
RT Piedmontese cattle";
RL Genome Res. 7:910-916(1997).

RP SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313.
RC STRAIN-HOLSTEIN; TISSUE-Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;

RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.

CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT
SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES

CC M. SEMIMEMBRANOSUS AND M. BICEPS FEMORIS; LOW LEVELS IN OTHER
CC HINDLIMB MUSCLES.

CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.
CC DAY 31 UP UNTIL LATE GESTATION.

CC -1- DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE
PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE
DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTESSE
CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASE IN
MUSCLE MASS OF 20-25%.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: AF019761; AAB81508.1; -
CC HSSP: P18075; 1BMP.

DR Interpro: IPR001839; TGF-beta.
DR Interpro: IPR001111; TGF-beta_N.

DR EMBL: AF019620; AAB86687.1; -
DR HSSP: P18075; 1BMP.

DR Interpro: IPR001839; TGF-beta.
DR Interpro: IPR001111; TGF-beta_N.

DR EMBL: AF019761; AAB81508.1; -
DR HSSP: P18075; 1BMP.

DR Interpro: IPR001839; TGF-beta.
DR Interpro: IPR001111; TGF-beta_N.

DR EMBL: AF019620; AAB86687.1; -
DR HSSP: P18075; 1BMP.

DR Interpro: IPR001839; TGF-beta.
DR Interpro: IPR001111; TGF-beta_N.

DR EMBL: AF019761; AAB81508.1; -
DR HSSP: P18075; 1BMP.

DR Interpro: IPR001839; TGF-beta.
DR Interpro: IPR001111; TGF-beta_N.

DR Pfam: PF00019; TGF-beta: 1.
 DR Pfam: PF00688; TGF-beta: 1.
 DR Pfam: PF000357; TGF-beta: 1.
 DR SMART: SM00204; TGF-beta: 1.
 DR PROSITE: PS00250; TGF-beta: 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
 FT SIGNAL 1 18
 FT PROPEP 19 266
 FT CHAIN 267 375
 FT DISULFID 281 340
 FT DISULFID 309 372
 FT DISULFID 313 374
 FT DISULFID 339 374
 FT CARBOHYD 47 47
 FT CARBOHYD 71 71
 FT VARIANT 94 94
 FT VARIANT 313 313
 FT CONFLICT 14 14
 FT SEQUENCE 375 AA; 42520 MW; E1B791AD92D4A9E6 CRC64;

Query Match 97.3%; Score 611; DB 1; Length 375;
 Best Local Similarity 97.2%; Pred. No. 7.1e-62;
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGECEVFLOKYPHTL 60
 DB 267 DFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGECEVFLOKYPHTL 326
 OY 61 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEOIYIGKIPAMVVDRCGS 109
 DB 327 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEOIYIGKIPAMVVDRCGS 375

RESULT 10
 GDFB_MOUSE STANDARD: PRT: 405 AA.
 ID GDFB_MOUSE STANDARD: PRT: 405 AA.
 AC 09U1W4; Q90X55; Q9R221;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11)
 GN GDF11 OR BMP11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99177155; PubMed=10075854;
 RA Ganer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R., Rosen V.;
 RA "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in xenopus embryos";
 RT Dev. Biol. 208:222-232(1999).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=129/SV;
 RC MEDLINE=99318097; PubMed=10391213;
 RA McPherron A.C., Lawler A.M., Lee S.-I.;
 RT "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11";
 RL Nat. Genet. 22:260-264(1999).
 RN [3]
 RP SEQUENCE OF 75-405 FROM N.A.
 RA MEDLINE=99173787; PubMed=10072786;
 RA Nakashima M., Toyono T., Akamine A., Joyner A.;
 RT "Expression of growth/differentiation factor 11, a new member of the BMP/TGF-beta superfamily during mouse embryogenesis";
 RL Mech. Dev. 80:185-189(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
 CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD, INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT DENTAL PULP AND BRAIN.
 CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC EMBL: AF100906; AAC72853.1; -;
 CC EMBL: AF100904; AAC72853.1; JOINED.
 CC EMBL: AF100905; AAC72853.1; JOINED.
 CC EMBL: AF028337; AAF21633.1; -;
 CC EMBL: AF028335; AAF21633.1; JOINED.
 CC EMBL: AF028336; AAF21633.1; JOINED.
 CC EMBL: AF092734; AAD05267.1; -;
 CC HSSP: P18075; IBMP.
 CC MGD: MGI:1338027; Gdf11.
 CC InterPro: IPR001839; TGF-beta.
 CC InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00019; TGF-beta: 1.
 DR Pfam: PF00688; TGF-beta: 1.
 DR ProDom: PD000357; TGF-beta: 1.
 DR SMART: SM00204; TGF-beta: 1.
 DR PROSITE: PS00250; TGF-beta: 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 296
 FT CHAIN 297 405
 FT DOMAIN 29 39
 FT DOMAIN 208 213
 FT DISULFID 311 370
 FT DISULFID 339 402
 FT DISULFID 343 404
 FT DISULFID 369 369
 FT CARBOHYD 92 92
 FT CARBOHYD 75 75
 FT CONFLICT 171 171
 FT CONFLICT 171 171
 FT SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;

Query Match 91.4%; Score 574; DB 1; Length 405;
 Best Local Similarity 89.0%; Pred. No. 1.2e-57;
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 DFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGECEVFLOKYPHTL 60
 DB 297 NFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGECEVFLOKYPHTL 356
 OY 61 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEOIYIGKIPAMVVDRCGS 109
 DB 357 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEOIYIGKIPAMVVDRCGS 405

RESULT 11
 GDFB_HUMAN STANDARD: PRT: 407 AA.
 ID GDFB_HUMAN STANDARD: PRT: 407 AA.
 AC 095390; Q9UID1; Q9UID2;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE growth/differentiation factor 11 precursor (Bone morphogenetic protein
 DE 11).
 GN GDF11 OR BMP11.
 OS Homo sapiens (Human).
 OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=99177155; PubMed=10075854;
 RA Garner L.W., Wolman N.M., Celeste A.J., Hattersley G., Hewick R.,
 RT Rosen V.;
 RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
 RT bud is a potent mesoderm inducer in Xenopus embryos.";
 RL Dev. Biol. 208:222-232(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99318097; PubMed=10391213;
 RA McPherron A.C., Lawler A.M., Lee S.-J.;
 RT "Regulation of anterior/posterior patterning of the axial skeleton by
 RT growth/differentiation factor 11.";
 RL Nat. Genet. 22:260-264(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
 CC IDENTIFY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
 CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>).
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF100907; AAC72852.1; -
 DR EMBL: AF028333; AAF21630.1; -
 DR EMBL: AF028334; AAF21631.1; -
 DR HSSP: P18075; 1BMP.
 DR MIM: 603936; -
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF000019; TGF-beta.1.
 DR Pfam: PF00688; TGFb.propeptide.1.
 DR ProDom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGFb.1.
 DR PROSITE: PS00250; TGF-BETA.1; 1.
 KW growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 298
 FT CHAIN 299 407
 FT DOMAIN 29 41
 FT DISULFID 210 215
 FT DISULFID 313 372
 FT DISULFID 341 404
 FT DISULFID 345 406
 FT DISULFID 371 371
 FT CARBOHYD 94 94
 FT SEQUENCE 407 AA: 45090 MW: 83FF48E363535BA6 CCK64;
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT GROWTH/DIFFERENTIATION FACTOR 11.
 FT POLY-ALA.
 FT POLY-GLY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT INTERCHAIN (BY SIMILARITY).
 FT N-LINKED (GLCNAC...) (POTENTIAL).

Query Match	91.48;	Score 574;	DB 1;	Length 407;
Best Local Similarity	89.08;	Pred. No. 1.2e-57;		
Matches 97;	Conservative 7;	Mismatches 5;	Indels 0;	Gaps 0

```

Db      299  NGLCDDHSSSSRCRRIPLYDFEFQMDWIIAPRIKANTCSGGCEMFQKTPHTL 358
Qy      61  VHOANPRGSAGCCPTTLMSPINMLYFNKGEQIIIGKIPAMVYDRCGS 109
Db      359  VQGANPRGSAGCCPTTKMSPINMLYFNDDKQIIIGKIPGMVYDRCGS 407

RESULT 12
GDF8_BRARE
ID      GDF8_BRARE      STANDARD:      PRT:      374 AA.
AC      042222:
DT      30-MAY-2000 (Rel. 39, Created)
DT      01-MAR-2002 (Rel. 41, Last sequence update)
DE      Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GDF8 OR MSTN.
OS      Brachydanio rerio (Zebrafish) (Zebra danio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC      Cypriniformes; Cyprinidae; Danio.
OX      NCBI_TaxID=7935;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Skletal muscle;
RX      MEDLINE=98024153; PubMed=9356471;
RA      McPherron A.C., Lee S.-J.;
RT      "Double muscling in cattle due to mutations in the myostatin gene.";
RL      Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC      -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC      MUSCLE GROWTH.
CC      -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      CC      the European Bioinformatics Institute. There are no restrictions on its
CC      CC      use by non-profit institutions as long as its content is in no way
CC      CC      modified and this statement is not removed. Usage by and for commercial
CC      CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019626; AAB86693.1; -.
DR      HSSP; P12643; 3BMP.
DR      ZFIN; ZDB-GENE-980415-165; gdf8.
DR      InterPro: IPR001839; TGF-beta.
DR      InterPro: IPR001111; TGFb_N.
DR      Pfam; PF00688; TGFb_propeptide.1.
DR      Prodom; PD000357; TGF-beta.1.
DR      SMART; SM00204; TGFb; 1.
DR      PROSITE; PS00250; TGF-BETA_1; 1.
KW      Growth factor; Cytokine; Glycoprotein; Signal.
FT      SIGNAL 1 22
FT      PROPEP 23 265
FT      CHAIN 266 374
FT      DISULFD 308 339
FT      DISULFD 312 373
FT      DISULFD 338 338
FT      CAROHD 72 72
FT      CAROHD 274 274
FT      SEQUENCE 374 AA; 42060 MW; 6302B6C686562576 CRC64;

```

Query Match 89.6%; Score 563; DB 1; Length 374;
Best Local Similarity 87.2%; Pred. No. 1, 9e-56;
Matches 95; Conservative 11; Mismatches 3; Indels 0; Gaps 0.

QY 1 DFGDDEHSTSRCCRRPLTVDFEAFGDMIIARRRYANTCGSECEVFLOKPPHTL 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 266 DSGLDDEHSSSRCCRRPLTVDFEFGDMIIARRRYANVCSCGDVNYLOKKPHTL 325

OY 61 VHOANRGSAGPCCPTPTLMSPTNMLYFNKGEOIYKIPAMVYDRCGS 109
 DB 326 VNRASPRGAGPCCPTPTKMSPTNMLYFNKGEOIYKIPSMVYDRCGS 374

RESULT 13

GDFB_RAT STANDARD: PRT: 345 AA.

AC 092217;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11) (Fragment).
 GN GDF11 OR BMP11.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dental pulp;
 RX MEDLINE=99137387; PubMed=10072786;
 A Nakashima M., Toyono T., Akamine A., Joyner A.;
 RT Expression of growth/differentiation factor 11, a new member of the BMP/TGFbeta superfamily during mouse embryogenesis.";
 RL Mech. Dev. 80:185-189(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 DR EMBL: AF092733; AAD05266.1; -.
 DR HSSP: P18075; BMP.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF000019; TGF-beta.1.
 DR Pfam: PF00688; TGFb.propeptide.1.
 DR Prodom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGFb.1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 DR Growth factor; cytokine; Glycoprotein.
 KW GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
 FT NON_TER 1
 FT PROPEP 1
 FT CHAIN 243
 FT DOVAIN 154
 FT DISULFID 257
 FT DISULFID 315
 FT CARBOHYD 38
 FT NON_TER 345
 FT SEQUENCE 345 AA: 39094 MW: 81D5B93FED6B0443 CRC64:

Query Match 83.9%; Score 527; DB 1; Length 345;

Best Local Similarity 87.4%; Pred. No. 2.1e-52;
 Matches 90; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 DEGLDDEHSTESRCRCRYLVDFEAFGMDWIAPKRYKANYCGSCCEVFLOKYPHTL 60
 DB 243 NLGLDDEHSTESRCRCRYLVDFEAFGMDWIAPKRYKANYCGSCCEVFLOKYPHTL 302
 OY 61 VHOANRGSAGPCCPTPTLMSPTNMLYFNKGEOIYKIPAMVY 103

DB 303 VHOANRGSAGPCCPTPTKMSPTNMLYFNKDOOIYKIPGMVY 345

RESULT 14

THBB_MOUSE STANDARD: PRT: 255 AA.

AC 004999; Q61277;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
 GN INHBB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE OF 1-234 FROM N.A.
 RC STRAIN=CBA X NMRI; TISSUE=Testis;
 RX MEDLINE=9534497; PubMed=7619733;
 RA Rittos O., Tuuri T., Eramaa M., Salnio K., Hilden K., Saxen L., Gilbert S.;
 RT Activin disrupts epithelial branching morphogenesis in developing glandular organs of the mouse.";
 RL Mech. Dev. 50:229-245(1995).
 RN (2)
 RP SEQUENCE OF 134-255 FROM N.A.
 RX MEDLINE=93321614; PubMed=8330535;
 RA Albano P.M., Groome N., Smith J.C.;
 RT Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.";
 RL Development 117:711-723(1993).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF ACTIVINS.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A-A AND BETA-B-B.
 CC -1- TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN, CUT EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 DR EMBL: X83376; CAA58290.1; -.
 DR EMBL: X69620; CAA49326.1; -.
 DR PIR: S31441; S31441.
 DR HSSP: P12643; 3BMP.
 DR GSD: MG1:96571; Inhbb.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF00019; TGF-beta.1.
 DR Prodom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGFb.1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 DR Growth factor; Hormone; Glycoprotein.
 KW NON_TER 1
 FT PROPEP 1
 FT CHAIN 140
 FT SEQUENCE 140 POTENTIAL.


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FT CHAIN 141 255 INHIBIN BETA B CHAIN.
FT DISULFID 144 152 BY SIMILARITY.
FT DISULFID 151 220 BY SIMILARITY.
FT DISULFID 180 252 BY SIMILARITY.
FT DISULFID 184 254 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 135 135 H -> D (IN REF. 2).
SQ SEQUENCE 255 AA: 29178 MW: 2524B21DC648D9A9 CRC64;

Query Match 38.4%; Score 241; DB 1; Length 255;
Best Local Similarity 42.4%; Pred. No. 4e-20;
Matches 50; Conservative 17; Mismatches 37; Indels 14; Gaps 6;

OY 3 GLDDEHSTESRCCRYPLTVDFEAFGW-DWIIAPRRYKANCSCGEFVFLQKYPH-----56
141 GLEDGRT--SLCCROGFIDFRIGNDWIIAPRTGYIGNCESCP-AVLAVPGSASS 197
57 -HRLVHQANPRG-SAGP---CCTPTLMSPIINMLYFNKGEQIIGKIPAVVDRCCG 109
198 FHFAVAVQYMRBGLNPGVNVSCIPTKLSSMSMLYFDEDEVNIVKRDVPMNIVECGCA 255

RESULT 15
DVR1_BRAE STANDARD; PRT: 355 AA.
AC P35621;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE DVR-1 protein precursor.
GN VGI OR DVR1 OR DVR-1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=94009920; Pubmed=8405668;
RA Heide K.A., Grunwald D.J.;
RT "The DVR-1 (Vg1) transcript of zebrafish is maternally supplied and
RT distributed throughout the embryo."
RL Dev. Biol. 159:418-426(1993).
CC -1- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
CC MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
CC SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
CC DISTRIBUTED AMONG ALL BLASTOMERES.
CC -1- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN
CC JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL
CC BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEAVAGE, BLASTULA AND
CC GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
CC GASTRULA.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; U00931; AAC27347.1; -.
CC DR HSSP; P12643; 3BP.
CC DR ZFIN; ZDB-GENE-980526-389; dvrl.
CC DR InterPro; IPR002400; GF_Cysknot.
CC DR InterPro; IPR001839; TGF_beta.
CC DR InterPro; IPR001111; TGFb_N.
CC DR Pfam; PF00019; TGF_beta; 1.

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DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGBB; 1.
DR PROSITE; PS00250; TGF_beta_1; 1.
KW Growth factor; Mitogen; Glycoprotein; signal.
FT SIGNAL 1 15
FT PROPEP 16 240
FT CHAIN 241 355
FT DISULFID 254 320
FT DISULFID 283 352
FT DISULFID 287 354
FT DISULFID 319 319
FT CARBOHYD 108 108
FT CARBOHYD 179 179
FT CARBOHYD 296 296
SQ SEQUENCE 355 AA: 40201 MW: 0BD5B9850EBFB222 CRC64;

Query Match 38.1%; Score 239; DB 1; Length 355;
Best Local Similarity 43.4%; Pred. No. 9.5e-20;
Matches 46; Conservative 16; Mismatches 36; Indels 8; Gaps 3;

OY 11 TESRCR-YPLTVDFEAFGW-DWIIAPRRYKANCSCGEFVFLQKYPHT-----LVH 62
249 TFSNVCKPRRLYIDPKDVGQMDWIIAPQGYLANVCHGCPPLSLNGTNNHAIQLTVH 308
63 QANRGSAQPCCTPTLMSPIINMLYFNKGEQIIGKIPAVVDRCCG 108
309 SFPKGTPOPCVPIKISPIISMLYDNDNVVLRHYEDMVVDECGC 354

Search completed: May 20, 2002, 09:24:50
Job time: 215 sec

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:20:50 ; Search time 24.89 Seconds
(without alignments)
757.591 Million cell updates/sec

Title: US-09-754-826-2
Perfect score: 628
Sequence: 1 DFGDDEHSTESRCRPL.....KEQIIVKIPAMVDRGCS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protein:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	622	99.0	162	6	09TSY2	09TSY2 sus scrofa
2	622	99.0	375	6	09GMB7	09GMB7 equus caball
3	622	99.0	375	6	095086	095086 macaca fasc
4	617	98.2	375	13	098SP0	098SP0 gallus gall
5	611	97.3	375	6	095M97	095M97 bos taurus
6	599	95.4	185	6	095M11	095M11 capra hircu
7	592	94.3	185	6	09M718	09M718 ovis aries
8	563	89.6	389	13	090YX0	090YX0 ictalurus p
9	560	89.2	385	13	090W05	090W05 sparus aura
10	557	88.7	373	13	09DD18	09DD18 salmo salar
11	557	88.7	373	13	090ZD2	090ZD2 oncorhynch
12	557	88.7	373	13	090ZD1	090ZD1 oncorhynch
13	557	88.7	376	13	098TR4	098TR4 oreochromis
14	557	88.7	376	13	090WC9	090WC9 morone saxa
15	557	88.7	376	13	090WC8	090WC8 morone amer
16	556	88.5	373	13	090W17	090W17 salmo salar

17	555	88.4	376	13	090W06	090W06 umbrina cir
18	552	87.9	377	13	098TR3	098TR3 morone chry
19	550	87.6	373	13	098UB3	098UB3 salvelinus
20	547	87.1	96	13	09W759	09W759 calina mos
21	522	83.1	107	6	09BG54	09BG54 sus scrofa
22	394	62.7	78	6	09XS86	09XS86 equus caball
23	311	49.5	191	13	098TR4	098TR4 perca flav
24	302	48.1	104	13	090Z79	090Z79 ictalurus p
25	294.5	46.9	598	5	09X622	09X622 drosophila
26	294.5	46.9	598	5	09YAF4	09YAF4 drosophila
27	286	45.5	58	6	095MF3	095MF3 sus scrofa
28	247	39.3	370	13	091350	091350 xenopus lae
29	238	37.9	395	13	09PWG6	09PWG6 anguilla ja
30	234.5	37.3	115	13	09DGE9	09DGE9 cyrinus ca
31	234.5	37.3	393	13	090261	090261 brachydanto
32	233.5	37.2	392	13	09PMR8	09PMR8 carassius a
33	232.5	37.0	115	13	09DGF1	09DGF1 cyrinus ca
34	232.5	37.0	115	13	09DGF0	09DGF0 cyrinus ca
35	232.5	37.0	115	13	09DGE6	09DGE6 oryzias lat
36	229.5	36.5	138	13	09MGT9	09MGT9 brachydanto
37	229.5	36.5	354	13	09YGV1	09YGV1 xenopus lae
38	226.5	36.1	349	5	097138	097138 brugia mala
39	223.5	35.6	361	5	096504	096504 branchiosto
40	223.5	35.6	411	5	090418	090418 branchiosto
41	222	35.4	373	13	090723	090723 gallus gall
42	222	35.4	373	13	098950	098950 gallus gall
43	216.5	34.5	399	13	09W753	09W753 xenopus lae
44	215.5	34.3	294	6	09BDW9	09BDW9 macaca fasc
45	215.5	34.3	447	6	09BDW8	09BDW8 cercopithec

ALIGNMENTS

RESULT 1
ID 09TSY2 PRELIMINARY; PRT: 162 AA.
AC 09TSY2;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE MROSTVITIN (FRAGMENT).
GS MSTN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20078370; Pubmed=10612246;
RA Stratil A., Kopecky M.;
RT "Genomic organization, sequence and polymorphism of the porcine
RT myostatin (GFET; MSTN) gene."
RL Anim. Genet. 30:468-470(1999).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AJ237920; CAB40844.1; .
DR HSSP: P18075; 1BMP
DR InterPro: IPR002400; GF_cyskn.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFB; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 162 AA; 18290 MW; FE353534512856E CRC64;

Query Match 99.0%; Score 622; DB 6; Length 162;
Best Local Similarity 99.1%; Pred. No. 4.1e-67;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 60
    |||||||
DB 54 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 113
OY 61 VHOANPRGSAGPCCTPTLMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 109
    |||||||
DB 114 VHOANPRGSAGPCCTPTKMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 162

RESULT 2
O9GM97 PRELIMINARY: PRT: 375 AA.
AC O9GM97:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSTATIN.
GN MSTN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
NN [1]
N- SEQUENCE FROM N.A.
NC STRAIN=THROUGHERED.
RA Hosoyama T., Yamamouchi K., Tojo H., Tachi C.;
RT "Molecular cloning of equine myostatin cDNA and serum level of
RT myostatin in horse.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL; AB033541; BABI6046.1; -.
DR HSSP; P18075; BMP.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42736 MW; 6F424ECBEE4D9936 CRC64;

Query Match 99.0%; Score 622; DB 6; Length 375;
Best Local Similarity 99.1%; Pred. No. 1e-66;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 60
    |||||||
DB 267 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 326
OY 61 VHOANPRGSAGPCCTPTLMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 109
    |||||||
DB 327 VHOANPRGSAGPCCTPTKMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 375

RESULT 3
O95J86 PRELIMINARY: PRT: 375 AA.
AC O95J86:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSTATIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
NN [1]
N- SEQUENCE FROM N.A.
NC TISSUE=GASTROCNEMIIUS;
RC
```

```
RA Smock S.L., Owen T.A.;
RT "Cloning of the open reading frame DNA for macaque fascicularis
RT (Cynomolgus macaque) myostatin (GDF8).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055750; AAL17640.1; -.
SQ SEQUENCE 375 AA; 42722 MW; 2149B46ACTD446E7 CRC64;

Query Match 99.0%; Score 622; DB 6; Length 375;
Best Local Similarity 99.1%; Pred. No. 1e-66;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 60
    |||||||
DB 267 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 326
OY 61 VHOANPRGSAGPCCTPTLMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 109
    |||||||
DB 327 VHOANPRGSAGPCCTPTKMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 375

RESULT 4
O98SP0 PRELIMINARY: PRT: 375 AA.
AC O98SP0:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSTATIN.
GN MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
NN [1]
N- SEQUENCE FROM N.A.
NC Zhang Y., Yang W., Zhu D.;
RT "Genomic structure and expression of the chicken GDF-8 during
RT development.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL; AF346599; AAK18000.1; -.
DR HSSP; P18075; BMP.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42717 MW; D980E286426E4DAF CRC64;

Query Match 98.2%; Score 617; DB 13; Length 375;
Best Local Similarity 98.2%; Pred. No. 4e-66;
Matches 107; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 60
    |||||||
DB 267 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANCSECEVFLOKYPHTHL 326
OY 61 VHOANPRGSAGPCCTPTLMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 109
    |||||||
DB 327 VHOANPRGSAGPCCTPTKMSPTNMLYFNKGEOIITGKIPAMVVDRCGCS 375

RESULT 5
O95N97 PRELIMINARY: PRT: 375 AA.
ID O95N97
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AC Q95N97;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSTATIN.
 GN GDF8.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-2143337; PubMed-11451380;
 RA Jeanplong F., Sharma M., Somers W.G., Bass J.J., Kambarur R.;
 RT "Genomic organization and neonatal expression of the bovine myostatin
 gene.";
 RT Mol. Cell. Biochem. 220:31-37(2001).
 EMBL; AF320998; AAG48116.1; -
 SO SEQUENCE 375 AA; 42551 MW; 84E1AB20650C05F6 CRC64;

Query Match 97.3%; Score 611; DB 6; Length 375;
 Best Local Similarity 97.2%; Pred. No. 2.1e-65;
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANKYSGCEEFYFLQKYPHTL 60
 DB 267 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANKYSGCEEFYFLQKYPHTL 326
 OY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEOIITYGKIPAMVYDRGC 109
 DB 327 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEOIITYGKIPAMVYDRGC 375

RESULT 6
 Q95N11 PRELIMINARY; PRT; 185 AA.

AC Q95N11;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSTATIN (FRAGMENT).
 GN MSTN.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9252;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lian Z., Pan Q., Chen H., Jin H., Li N.;
 RT "Cloning of intron 2 of the myostatin gene in goat.";
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY032689; AAK49790.1; -
 FT NON_TER 1 185
 FT SEQUENCE 185 AA; 20953 MW; 03675B386E9D4D4 CRC64;

Query Match 95.4%; Score 599; DB 6; Length 185;
 Best Local Similarity 96.3%; Pred. No. 2.8e-64;
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANKYSGCEEFYFLQKYPHTL 60
 DB 79 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANKYSGCEEFYFLQKYPHTL 138
 OY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEOIITYGKIPAMVYDRGC 107
 DB 139 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEOIITYGKIPAMVYDRGC 185

RESULT 7
 Q9MZ18 PRELIMINARY; PRT; 185 AA.

AC Q9MZ18;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSTATIN (FRAGMENT).
 GN MSTN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lian Z., Jin H., Li N.;
 RT "Cloning of intron 2 of the myostatin gene in sheep.";
 RT Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF266758; AAF78069.1; -
 DR HSSP; P12643; 3BP.
 DR InterPro; IPR001839; TGF-beta.
 DR Pfam; PF00019; TGF-beta; 1.
 DR ProDom; PD000357; TGF-beta; 1.
 DR SMART; SM00204; TGF-beta; 1.
 DR PROSITE; PS00250; TGF-BETA; 1.
 KW Glycoprotein.
 FT NON_TER 1 185
 FT SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;

Query Match 94.3%; Score 592; DB 6; Length 185;
 Best Local Similarity 95.3%; Pred. No. 1.9e-63;
 Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANKYSGCEEFYFLQKYPHTL 60
 DB 79 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANKYSGCEEFYFLQKYPHTL 138
 OY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEOIITYGKIPAMVYDRGC 107
 DB 139 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEOIITYGKIPAMVYDRGC 185

RESULT 8
 Q90YYO PRELIMINARY; PRT; 389 AA.

AC Q90YYO;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSTATIN.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Siluriformes; Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kocabas A.M., Liu Z.J.;
 RT "Molecular characterization and expression of the myostatin gene from
 channel catfish (Ictalurus punctatus).";
 RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF396747; AAK84666.1; -
 SO SEQUENCE 389 AA; 43600 MW; 569F9B92B7E9E173 CRC64;

Query Match 89.6%; Score 563; DB 13; Length 389;
 Best Local Similarity 89.7%; Pred. No. 1.3e-59;
 Matches 96; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

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QY 3 GLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHLVH 62
DB 283 GLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHLVH 342
QY 63 QANPRGSAGPCCTPTLMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 109
DB 343 KANPRGTAGPCTPTKMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 389

RESULT 9
ID 090M05 PRELIMINARY; PRT: 385 AA.
AC 090M05.
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSTATIN.
OS Sparus aurata (gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Maccacozzo L., Bargelloni L., Radaelli G., Mascarello F.,
RA Patarrello T.;
RT "Characterization of the myostatin gene in the gilthead seabream,
RT Sparus aurata: sequence, genomic structure, and expression pattern.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF288448; AAK53545.1; -
DR EMBL: AF288447; AAK53544.1; -
SQ SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;

Query Match 89.2%; Score 560; DB 13; Length 385;
Best Local Similarity 89.0%; Pred. No. 3e-59;
Matches 97; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DGLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHL 60
DB 277 DGLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHL 336
QY 61 VQANPRGSAGPCCTPTLMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 109
DB 337 VKNANPRGSAGPCCTPTKMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 385

RESULT 10
ID 09DD18 PRELIMINARY; PRT: 373 AA.
AC 09DD18.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSTATIN PRECURSOR.
OS GDF-8.
OC Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
RT expressed in a variety of tissues.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Andersen O.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
RA Andersen O.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
RT expressed in a variety of tissues.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AJ297267; CAC19541.2; -
DR EMBL: AJ316006; CAC59700.1; -
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_M.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 265 373 MYOSTATIN.
SQ SEQUENCE 373 AA; 41896 MW; C641D71D83E66C4D CRC64;

Query Match 88.7%; Score 557; DB 13; Length 373;
Best Local Similarity 88.1%; Pred. No. 6.7e-59;
Matches 96; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DGLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHL 60
DB 265 DGLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHL 324
QY 61 VQANPRGSAGPCCTPTLMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 109
DB 325 VKNANPRGTAGPCTPTKMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 373

RESULT 11
ID 090ZD2 PRELIMINARY; PRT: 373 AA.
AC 090ZD2.
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSTATIN 1.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Rescan P.-Y., Jutel I., Ralliere C.;
RT "Two myostatin genes are differentially expressed in myotomal muscle
RT of the trout (Oncorhynchus mykiss).";
RL J. Exp. Biol. 0:0-0(2001).
DR EMBL: AF273035; AAK71707.1; -
SQ SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;

Query Match 88.7%; Score 557; DB 13; Length 373;
Best Local Similarity 88.1%; Pred. No. 6.7e-59;
Matches 96; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DGLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHL 60
DB 265 DGLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTHL 324
QY 61 VQANPRGSAGPCCTPTLMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 109
DB 325 VKNANPRGTAGPCTPTKMSPINMLYFNKKEQIIYGIKIPAMVVDRCGS 373

RESULT 12
ID 090ZD1 PRELIMINARY; PRT: 373 AA.
AC 090ZD1.

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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:20:25 ; Search time 16.7 Seconds
(without alignments)
627.170 Million cell updates/sec

Title: US-09-754-826-2
Perfect score: 628
Sequence: 1 DFGDCDEHSTESRCRYPL.....KEQIIVGKIPAMVVDRCGCS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247	39.3	370	2	I51199
2	241	38.4	255	2	I48235
3	241	38.4	411	2	B41398
4	237.5	37.8	115	2	PN0506
5	235	37.4	349	1	WFP058
6	235	37.4	407	1	A40150
7	235	37.4	408	2	S50899
8	234.5	37.3	393	2	I50103
9	232.5	37.0	115	2	PN0505
10	225.5	35.9	207	2	S37618
11	225.5	35.9	513	1	BMH06
12	223.5	35.6	510	2	A54798
13	212.5	33.8	313	2	I51284
14	212.5	33.8	360	2	A29619
15	212.5	33.7	125	2	S43295
16	211.5	33.7	352	2	JC5366
17	211.5	33.7	352	2	S70580
18	211.5	33.6	436	2	B55452
19	211	33.6	373	2	PM0042
20	210.5	33.5	413	2	JC4862
21	210.5	33.5	424	1	WFP058
22	210.5	33.5	424	1	S31440
23	210.5	33.5	424	1	B40905
24	210.5	33.5	425	1	S50898
25	210.5	33.5	425	2	I47072
26	210.5	33.5	426	1	B24248
27	210.5	33.5	426	2	JH0690
28	209.5	33.4	367	2	JC4151
29	209.5	33.4	431	1	BMH07

30	208.5	33.2	352	2	JC2466	inhibin beta-C cha
31	207.5	33.0	151	2	S43296	bone morphogenetic
32	207.5	33.0	430	2	J01184	osteogenic protein
33	206.5	32.9	495	2	S43294	bone morphogenetic
34	206.5	32.9	501	2	A53452	cartilage-derived
35	206.5	32.9	501	2	JC2347	growth/differentia
36	205.5	32.7	402	2	A45056	osteogenic protein
37	204.5	32.6	350	2	JC5241	activin beta B cha
38	204	32.5	350	2	T25451	transforming growt
39	204	32.5	393	2	S37073	bone morphogenetic
40	204	32.5	394	2	S45355	bone morphogenetic
41	204	32.5	396	1	BMH02	bone morphogenetic
42	204	32.5	398	2	JH0688	bone morphogenetic
43	204	32.5	398	2	JH0687	bone morphogenetic
44	203	32.3	353	2	I50607	bone morphogenetic
45	201.5	32.1	409	2	S01825	transforming growt

ALIGNMENTS

RESULT 1
I51199
activin beta B subunit - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I51199
R:Dohmann, C.E.; Hemmati-Briyvanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melt
Dev. Biol. 157, 474-483, 1993
A>Title: Expression of activin mRNA during early development in Xenopus laevis.
A:Reference number: I51199; M01D:93273083
A:Accession: I51199
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-370 <DOH>
A:Cross-references: GB:S61773; MID:q386027; PIDN:AAB26863.1; PID:q386028
C:Superfamily: inhibin

Query Match 39.3%; Score 247; DB 2; Length 370;

Best Local Similarity 41.5%; Pred. No. 3.1e-19;

Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

OY 3 GLDCDEHSTESRCRYPLVDFEAFGW-DWIIAPKRYKAVCSGCEPFLQKYP----- 56

Db 256 GLDCDGHF--NLCCRQFYIDFRLIGNMDWIIAPAGYGVKCSGSCF-ATLAVPGSASS 312

OY 57 -HTHLVHQANPR---GSAGPCCTPTLMSPIINMLYFNGKEQIIVGKIPAMVVDRCGCS 109

Db 313 FHTAVVAVQVBMRCGLNPQTVNSCCIPTKLSTPMSMLYFDEYNIYKRDVPMIVDCEGCA 370

RESULT 2

I48235
inhibin beta-B chain - mouse (fragment)

N:Alternate names: activin bB chain

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999

C:Accession: I48235; I48266; S31441

R:Rlyvos, O.; Tuurti, T.; Eramaa, M.; Salnio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F.

Mech. Dev. 50, 229-245, 1995

A>Title: Activin disrupts epithelial branching morphogenesis in developing glandular

A:Reference number: I48235; M01D:95344997

A:Accession: I48235

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-234 <RES>

A:Cross-references: EMBL:X83376; MID:g603571; PIDN:CAAS8290.1; PID:g603572

R:Albanio, R.M.; Groome, N.; Smith, J.C.

Development 117, 711-723, 1993

A>Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cel

A:Reference number: I48243; M01D:93321614

A:Accession: I48266


```

A:Title: Activin B: precursor sequences, genomic structure and in vitro activities.
A:Reference number: A40150; MUID: 90114200
A:Accession: A40150
A:Molecule type: DNA
A:Residues: 1-407 <MAS>
A:Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
R:Masou, A.J.; Niall, H.D.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A:Title: Structure of two human ovarian inhibins.
A:Reference number: A90123; MUID:86186863
A:Accession: C24248
A:Molecule type: mRNA
A:Residues: 55-407 <MA2>
A:Cross-references: GB:M3437; NID:g186416; PIDN:AAA59169.1; PID:g186417
R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
Mol. Endocrinol. 3, 939-948, 1989
A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
A:Reference number: A40156; MUID:89295443
A:Accession: A40156
A:Molecule type: mRNA
A:Residues: 22-46, 'A', '48-407 <FEN>
A:Cross-references: GB:M31632
A:Experimental source: testis
R:Schmeizler, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N.
Biochim. Biophys. Acta 1039, 135-141, 1990
A:Title: Purification and characterization of recombinant human activin B.
A:Reference number: S10751; MUID:90304183
A:Accession: S10751
A:Molecule type: protein
A:Residues: 293-284, 'GX', 297-302, 'XX', 305-307 <SCH>
C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
bin beta-A and beta-B, respectively.
C:Genetics:
A:Gene: GDB:INHBB
A:Cross-references: GDB:119347; OMIM:147390
A:Map position: 2cen-2q13
C:Superfamily: inhibin
C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-293/Domain: propeptide #status predicted <PRO>
F:293/Product: inhibin beta-B chain #status predicted <MA7>
F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.4%, Score 235, DB 1; Length 407;
Best Local Similarity 39.8%; Pred. NO. 7e-18;
Matches 47; Conservative 18; Mismatches 39; Indels 14; Gaps 5;

Oy 3 GDDCGHSHSCCCYPPLTVDPEAFGW-DWITAPRYKANYCSCGECEVPLOKYP----- 56
Db 293 GLECGRT--NLCCKQGFIDRLIGMNDWIIAPRGTYGNICEGSCP-AYLAGVGSASS 349
Oy 57 -HTHLVHOANPR-----GSAGPCCTPTLMSPIINMLYFNKGEQIITYIKIPAMVVDRCGS 109
Db 350 FHTAVVNGYRMGLNPGVNVNSCCIPTKLSTSMLEYFDEDEVINIKRDVDMIVEEGCA 407

RESULT 7
S50899
betab inhibin precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S50899
R:Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B)
Y-DNAse I footprinting.
A:Reference number: S50897; MUID:95112839
A:Accession: S50899
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-408 <THO>
A:Cross-references: EMBL:U16240

```

C:Genetics: 151/1
A:introns: 151/1
C:Superfamily: inhibin

Query Match 37.4%; Score 235; DB 2; Length 408;
Best Local Similarity 39.8%; Pred. No. 7e-18;
Matches 47; Conservative 18; Mismatches 39; Indels 14; Gaps 5;

OY 3 GUDCEHSTESRCCRYPLTVDFEAFGW-DWIIAPRYKANYCSGCECFVFLQKYP----- 56
||:|:| : ||| || ||||| | ||| : |
Db 294 GLECCGR- -NLCRQOPFIDFRLIGWMDWIIAPGYGVNCGECCP-AYLAGVPGSASS 350
||:|:| : ||| || ||||| | ||| : |

OY 57 -HTHLVHOANPR---GSAGPCCTPTLMSPTNMLTFNGKEQIIYGIKIPAMVVDRCGS 109
||:|:| : ||| || ||||| | ||| : |
Db 351 FHTAVVNOYRMKGMLNPGIVNNSCCIFPTKLTSMMLTFDEDEYNIVKRDVNMIVEECGCA 408
||:|:| : ||| || ||||| | ||| : |

RESULT 8
150103
activin beta B - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: 150103
R:Miltbrodt, J.; Rosa, F.M.
Genes Dev. 8, 1448-1462, 1994
A>Title: Distribution of mesoderm and axis formation in fish by ectopic expression of a
A:Reference number: 150103; MUID:95011555
A:Accession: 150103
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-393 <WIT>
A:Cross-references: EMBL:X76051; NID:9516356; PIDN:CAAS3636.1; PID:9516357
C:Genetics:
A:Gene: ZactbetaB
C:Superfamily: inhibin

Query Match 37.3%; Score 234.5; DB 2; Length 393;
Best Local Similarity 39.8%; Pred. No. 7.7e-18;
Matches 47; Conservative 18; Mismatches 40; Indels 13; Gaps 5;

OY 3 GUDCEHSTESRCCRYPLTVDFEAFGW-DWIIAPRYKANYCSGCECFVFLQKYP----- 56
||:|:| : ||| || ||||| | ||| : |
Db 278 GLECCGN- -GLCCRQOPFIDFRLIGWMDWIIAPGYGVNCGECCP-AYMAGVPGSASS 335
||:|:| : ||| || ||||| | ||| : |

OY 57 -HTHLVHOANPR---GSAGPCCTPTLMSPTNMLTFNGKEQIIYGIKIPAMVVDRCGS 109
||:|:| : ||| || ||||| | ||| : |
Db 336 FHTAVVNOYRMKGMSPGSVNSCCIFPTKLTSMMLTFDEDEYNIVKRDVNMIVEECGCA 393
||:|:| : ||| || ||||| | ||| : |

RESULT 9
PN0505
activin beta B-1 chain - goldfish (fragment)
N:Alternate names: gact 2
C:Species: Carassius auratus (goldfish)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0505
R:Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
Biochem. Biophys. Res. Commun. 193, 711-717, 1993
A>Title: Cloning and sequencing of goldfish activin subunit genes: strong structural
A:Reference number: PN0504; MUID:93290666
A:Accession: PN0505
A:Molecule type: DNA
A:Residues: 1-115 <GEW>
C:Superfamily: inhibin

Query Match 37.0%; Score 232.5; DB 2; Length 115;
Best Local Similarity 40.2%; Pred. No. 3.6e-16;
Matches 47; Conservative 16; Mismatches 41; Indels 13; Gaps 5;

OY 3 GUDCEHSTESRCCRYPLTVDFEAFGW-DWIIAPRYKANYCSGCECFVFLQKYP----- 56

Db 1 GLECD-GTGGGLCCROQFYIDRLIGWMDWIIAPAGYGNCEGSCP-AYMAGVPCSSASS 58
OY 57 -FTHLVHQAANPR---GSAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVVDRCGC 108
Db 59 FHTAVVNOYRMKGISIPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPMNIVECCGC 115

RESULT 10

S37618
vgr protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
C:Accession: S37618
R:Sauremann, U.; Meyerann, R.; Schluesener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
A:Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning
A:Reference number: S37618; MUID:93085758
A:Accession: S37618
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <SAU>
C:Cross-references: EMBL:X58830; NID:957475; PIDN:CAA41634.1; PID:957476
Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser
C:Superfamily: Inhibin

Query Match 35.9%; Score 225.5; DB 2; Length 207;
Best Local Similarity 41.4%; Pred. No. 3.8e-17;
Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2;

OY 5 DCDENHSTRCRCRYPLTVDFEAFGW-DWIIAPRRYKANYCGSECFEVLQKKYPHTH---- 59
Db 96 DYNSELKTKACKKHELYVSFDLGMQDWIIAPRGYANAYCDEGSPPLNAHNNATNHAIV 155
OY 60 --LVHQAANRGSAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVVDRCGC 108
Db 156 QTLVHLMNPEYVPRPCCAPTKLNAISLVLFDDNSNVILKKRYNMVVRACGC 206

RESULT 11

BHM06
bone morphogenetic protein 6 precursor - human
C:Species: Homo sapiens (man)
C:Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: B39263
R:Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A:Title: Identification of transforming growth factor beta family members present in bone
A:Reference number: A39263; MUID:91088608
A:Accession: B39263
A:Molecule type: mRNA
A:Residues: 1-513 <CEU>
C:Cross-references: GB:M60315; GB:M38694; NID:g339561; PIDN:AAA36737.1; PID:g339562
C:Genetics:
A:Gene: GDB:BMP6
A:Cross-references: GDB:127596; OMIM:112266
A:Map position: 6pter-6qter
C:Superfamily: Inhibin
C:Keywords: bone; glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-374/Domain: propeptide #status predicted <PRO>
F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
F:241,269,386,404,454/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 35.9%; Score 225.5; DB 1; Length 513;
Best Local Similarity 41.4%; Pred. No. 9.7e-17;
Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2;

OY 5 DCDENHSTRCRCRYPLTVDFEAFGW-DWIIAPRRYKANYCGSECFEVLQKKYPHTH---- 59
Db 402 DYNSELKTKACKKHELYVSFDLGMQDWIIAPRGYANAYCDEGSPPLNAHNNATNHAIV 461

OY 60 --LVHQAANRGSAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVVDRCGC 108
Db 462 QTLVHLMNPEYVPRPCCAPTKLNAISLVLFDDNSNVILKKRYNMVVRACGC 512

RESULT 12

A54798
Vg-1-related protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C:Accession: A54798; A33925; S47442
R:Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994
A:Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral b
A:Reference number: A54798; MUID:94375533
A:Accession: A54798
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-510 <GIN>
A:Cross-references: EMBL:X80992; NID:9530729; PIDN:CAA56917.1; PID:9530730
R:Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A:Title: Vgr-1, a mammalian gene related to xenopus Vg-1, is a member of the transfor
A:Reference number: A33925; MUID:89282810
A:Accession: A33925
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-74, 'K', 76-85, 'P', 87-510 <LYO>
A:Cross-references: GB:J04566; NID:g202352; PIDN:AAA40548.1; PID:g202353
C:Superfamily: Inhibin

Query Match 35.6%; Score 223.5; DB 2; Length 510;
Best Local Similarity 41.4%; Pred. No. 1.6e-16;
Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2;

OY 5 DCDENHSTRCRCRYPLTVDFEAFGW-DWIIAPRRYKANYCGSECFEVLQKKYPHTH---- 59
Db 399 DYNSELKTKACKKHELYVSFDLGMQDWIIAPRGYANAYCDEGSPPLNAHNNATNHAIV 458
OY 60 --LVHQAANRGSAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVVDRCGC 108
Db 459 QTLVHLMNPEYVPRPCCAPTKLNAISLVLFDDNSNVILKKRYNMVVRACGC 509

RESULT 13

I51284
bone morphogenetic protein-7 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C:Accession: I51284
R:Houston, B.; Thorp, B.H.; Burt, D.W.
J. Mol. Endocrinol. 13, 289-301, 1994
A:Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick
A:Reference number: I51284; MUID:9520473
A:Accession: I51284
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313 <HOU>
A:Cross-references: GB:S77477; NID:g957233; PIDN:AAA33846.1; PID:g957234
C:Superfamily: Inhibin

Query Match 33.8%; Score 212.5; DB 2; Length 313;
Best Local Similarity 40.3%; Pred. No. 1.5e-15;
Matches 48; Conservative 14; Mismatches 44; Indels 13; Gaps 5;

OY 2 FGID--CDENHSTSR--CCRYPLTVDFEAFGW-DWIIAPRRYKANYCGSECFEVLQKKYP 56
Db 195 FGMSNIAENSSDDQACCKKHELYVSFDLGMQDWIIAPRGYANAYCDEGCAF-P-LNSYM 253
OY 57 HT-----HLVHQAANRGSAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVVDRCGC 108

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: May 20, 2002, 09:20:25 ; Search time 30.38 Seconds
(Without alignments)
398.520 Million cell updates/sec

Title: US-09-754-826-2
Perfect score: 628
Sequence: 1 DFGIDCDHSTESRCRYPL.....KEQIYKIPAMVDRCCGS 109

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622	99.0	109	22	AAB20141 Human growth diffe
2	622	99.0	126	15	AAR63161 Mouse growth diffe
3	622	99.0	126	19	AAM69883 Murine growth diffe
4	622	99.0	126	20	AAI15386 C-terminal region
5	622	99.0	126	22	AAB73182 Ratine GDP-8 #1.
6	622	99.0	130	22	AAB73189 Murine GDP-8. Rattus
7	622	99.0	160	22	AAB20153 Growth differentia
8	622	99.0	226	22	AAB73188 Chicken GDP-8. Ga
9	622	99.0	254	22	AAB20152 Growth differentia
10	622	99.0	362	22	AAB20132 Turkey growth diffe
11	622	99.0	375	15	AAR63160 Human growth diffe

12	622	99.0	375	19	AAM69888 Chicken growth dif
13	622	99.0	375	19	AAM69891 Pig growth diffe
14	622	99.0	375	19	AAM69885 Human growth diffe
15	622	99.0	375	19	AAM69860 Human growth diffe
16	622	99.0	375	20	AAI33838 Amino acid sequenc
17	622	99.0	375	20	AAI33839 Amino acid sequenc
18	622	99.0	375	20	AAI33840 Amino acid sequenc
19	622	99.0	375	20	AAI33841 Amino acid sequenc
20	622	99.0	375	20	AAI33843 Amino acid sequenc
21	622	99.0	375	20	AAI33844 Amino acid sequenc
22	622	99.0	375	20	AAI33937 Amino acid sequenc
23	622	99.0	375	20	AAI33938 Amino acid sequenc
24	622	99.0	375	20	AAI33932 Amino acid sequenc
25	622	99.0	375	20	AAI33935 Amino acid sequenc
26	622	99.0	375	20	AAI33189 Human GDP-8 protei
27	622	99.0	375	20	AAI33192 Chicken GDP-8 prot
28	622	99.0	375	20	AAI31194 Turkey GDP-8 prote
29	622	99.0	375	20	AAI97887 Human myofastatin.
30	622	99.0	375	21	AAI21087 Human GDP-8. Homo
31	622	99.0	375	21	AAI92035 Human GDP-8. Homo
32	622	99.0	375	21	AAI77566 Human growth diffe
33	622	99.0	375	22	AAI73187 Human GDP-8 #2. H
34	622	99.0	375	22	AAI20131 Human growth diffe
35	622	99.0	375	22	AAB20133 Chicken-growth dif
36	622	99.0	375	22	AAB20138 Pig growth diffe
37	622	99.0	376	15	AAR63159 Mouse growth diffe
38	622	99.0	376	15	AAM69889 Rat growth diffe
39	622	99.0	376	19	AAM30689 Murine growth diffe
40	622	99.0	376	20	AAI33837 Amino acid sequenc
41	622	99.0	376	20	AAI33842 Amino acid sequenc
42	622	99.0	376	20	AAI33930 Amino acid sequenc
43	622	99.0	376	20	AAI33931 Amino acid sequenc
44	622	99.0	376	20	AAI31193 Rat GDP-8 protein.
45	622	99.0	376	20	AAI31188 Murine GDP-8 prote

ALIGNMENTS

RESULT 1	
AAB20141	standard; Protein; 109 AA.
XX	
AC	AAB20141:
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Human growth differentiation factor 8 C-terminal region.
XX	
KW	Growth differentiation factor 8; GDP-8; myostatin; down-regulation;
KW	vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutlein.
XX	
OS	Homo sapiens.
OS	Synthetic.
PN	W0200105820-A2.
XX	
PD	25-JAN-2001.
XX	
PE	20-JUL-2000; 200OWO-DK0413.
XX	
PR	20-JUL-1999; 99DK-0001014.
XX	
PR	26-JUL-1999; 99US-0145275.
XX	
PA	(MEBI-) M & E BIOTECH AS.
XX	
PI	Halkier T, Moutlsen S, Klysnar S;
XX	
DR	WPI, 2001-112680/12.
XX	
PT	Increasing the muscle mass of animals used in meat production by down
PT	regulating growth differentiation factor 8 (GDP-8) activity in the
PT	animal through induction of anti-GDP-8 antibody production

xx Claim 17; Page 93-94; 110pp; English.
 CC The present sequence comprises the 109 amino acid residue
 CC C-terminal region of human growth differentiation factor 8
 CC (GDF-8), i.e. residues 267-375 of the full-length protein (see
 CC AAB0131). The homodimer of this region is thought to be the
 CC biologically active form of GDF-8. It is an object of the
 CC invention to produce a recombinant therapeutic vaccine capable of
 CC effecting down-regulation of GDF-8 in order to increase the muscle
 CC growth rate of farm animals. Variants of GDF-8 (see AAB0145-53)
 CC are provided that are capable of breaking autotolerance against
 CC autologous GDF-8. These comprise the C-terminal portion of human
 CC GDF-8 in which a portion of the native sequence is replaced by a
 CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
 CC P2 or P30. The high number (9) of Cys residues in the C-terminal
 CC region limits the possible sites in which the T-cell epitope can be
 CC positioned without major disturbance of the native 3-dimensional
 CC structure of the protein. Nucleic acids encoding the GDF-8 variants
 CC can be used for genetic immunisation of the animals. Down-regulation
 CC of GDF-8 activity can increase muscle mass by up to at least 45% in
 CC cattle, pigs and poultry used for meat production, reducing the need
 CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to
 CC treat human diseases such as cancer cachexia where muscle atrophy is
 CC pronounced and for patients suffering from acute and chronic heart
 CC failure.

CC Sequence 109 AA:

Query Match 99.0%; Score 622; DB 22; Length 109;
 Best Local Similarity 99.1%; Pred. No. 1.3e-59;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DGLDDEHSTSRRCRYPLTVDFEAFGMDWIAPRKRYKANCSCGEFVFLQKYPHTL 60
 Db 1 dfgldcdensstsrccrypltdvdfefgwdwllaprkrykancscgecfvflqkyphtl 60
 OY 61 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
 Db 61 vhaqnpgrgsagpcctptlmspinmlyfngkeqlygkipamvvdrcgcs 109

RESULT 2

AAR63161 AAR63161 standard; Protein; 126 AA.

AC AAR63161;

DT 23-JUN-1995 (first entry)

Mouse growth differentiation factor-8 partial sequence.

KM Growth differentiation factor-8; GDF-8; cell proliferation;
 KM adipocyte; obesity; transforming growth factor-beta.

OS Mus musculus.

PN WO9421681-A.

PD 29-SEP-1994.

PF 18-MAR-1994; 94WO-US03019.

PR 19-MAR-1993; 93US-0033923.

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.

PT Lee S, McPherron AC;

DR WPI: 1994-316943/39.

DR Q-PSDB: Q76380.

XX

PT New growth differentiation factor 8 - useful for treatment and
 PT diagnosis of cell proliferative disorders esp. of muscle.

PS Disclosure; Page 41; 84pp; English.

CC GDF-8 can be used to maintain cells before transplantation; to
 CC improve efficiency of cell fusion and to treat obesity or diseases
 CC related to abnormal adipocyte proliferation.

SO Sequence 126 AA:

Query Match 99.0%; Score 622; DB 15; Length 126;
 Best Local Similarity 99.1%; Pred. No. 1.6e-59;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DGLDDEHSTSRRCRYPLTVDFEAFGMDWIAPRKRYKANCSCGEFVFLQKYPHTL 60
 Db 18 dfgldcdensstsrccrypltdvdfefgwdwllaprkrykancscgecfvflqkyphtl 77
 OY 61 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
 Db 78 vhaqnpgrgsagpcctptlmspinmlyfngkeqlygkipamvvdrcgcs 126

RESULT 3

AAW69883 AAW69883 standard; Protein; 126 AA.

AC AAW69883;

DT 07-DEC-1998 (first entry)

DE Murine growth differentiation factor-8 C-terminal fragment.

KM Growth differentiation factor-8; GDF-8; mouse; transgenic animal;
 KM transforming growth factor-beta; muscle; meat; inhibitor; obesity;
 KM neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
 KM therapy.

OS Mus sp.

PN WO9833887-A1.

PD 06-AUG-1998.

PF 05-FEB-1998; 98WO-US02479.

PR 23-MAY-1997; 97US-0862445.

PR 05-FEB-1997; 97US-0795071.

PR 28-APR-1997; 97US-0847910.

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PT Lee S, McPherron AC;

DR WPI: 1998-437444/37.

DR N-PSDB: AAW45809.

XX Transgenic animals with gene for growth differentiation factor-8

PT disrupted - have increased muscle and reduced cholesterol contents,
 PT also use of GDF-8 inhibitors for treating cancer, obesity,
 PT neuromuscular disease

PS Example 2; Page 58; 125pp; English.

XX This is the amino acid sequence of the C-terminal portion of mouse

XX

CC


```

XX 19-AUG-1999; 99US-0378238.
PR (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA
XX Lee S, McPherron AC;
XX WPI: 2001-211209/21.
DR N-PSDB: AAF63547.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia
PT
PS Example 2; Fig 2; 124pp; English.
XX
CC The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a GDF-8 protein,
CC which was isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), muscledenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.
CC
XX Sequence 126 AA:
SO
Query Match 99.0%; Score 622; DB 22; Length 126;
Best Local Similarity 99.1%; Pred. No. 1.6e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIAPRKRYKANGSGCEVFLOKYPHTL 60
DB 18 dfgldcdenstescrcrypltvdfefagwdwllapkrkykangsgcevfllqkyphtl 77
QY 61 VHOAMPKRSAGPCPCPTLMSPTNMLYFNKGKQIIVGKIPAMVVDRCGS 109
DB 78 vhoampkrsagpcpcptlmsptnmllyfngkqilygkipamvvdrcgs 126
RESULT 6
AAB73189
ID AAB73189 standard; Protein: 130 AA.
AAB73189;
DT 11-MAY-2001 (first entry)
XX
DE Rat GDF-8.
XX
KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; muscledenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.
XX
OS Rattus sp.
XX
PN WO200112777-A2.
XX
PJ 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22884.
XX
PR 19-AUG-1999; 99US-0378238.
XX

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PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Lee S, McPherron AC;
XX WPI: 2001-211209/21.
DR N-PSDB: AAF63555.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia
PT
PS Example 9; Fig 2; 124pp; English.
XX
CC The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a GDF-8 protein,
CC which was isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), muscledenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.
CC
XX Sequence 130 AA:
SO
Query Match 99.0%; Score 622; DB 22; Length 130;
Best Local Similarity 99.1%; Pred. No. 1.6e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIAPRKRYKANGSGCEVFLOKYPHTL 60
DB 22 dfgldcdenstescrcrypltvdfefagwdwllapkrkykangsgcevfllqkyphtl 81
QY 61 VHOAMPKRSAGPCPCPTLMSPTNMLYFNKGKQIIVGKIPAMVVDRCGS 109
DB 82 vhoampkrsagpcpcptlmsptnmllyfngkqilygkipamvvdrcgs 130
RESULT 7
AAB20153
ID AAB20153 standard; Protein: 160 AA.
AAB20153;
XX
AC AAB20153;
XX
DT 30-APR-2001 (first entry)
XX
DE Growth differentiation factor 8 AutoVac construct GDF-8 ext.
XX
KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
KW T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW cardiacant; human; mutant; mutlein.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Clostridium tetani.
OS Synthetic.
XX
XX
FH Key
FH Region
FT 1..15
FT /note= "identical to residues 215-230 of human
FT GDF-8"
FT
FT Region
FT 16..36
FT /note= "tetanus toxoid p30 epitope"
FT
FT Region
FT 37..51
FT /note= "tetanus toxoid p2 epitope"
FT
FT Region
FT 52..160
FT /note= "identical to residues 267-375 of human
FT GDF-8"
FT

```


KM T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
 KW cardant; human, mutant; mutein.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Clostridium tectani.
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FT Region 1..109
 FT /note= "109 C-terminal residues of human GDF-8"
 FT Region 110..124
 FT /note= "tctanus toxoid P2 epitope"
 FT Region 125..145
 FT /note= "tctanus toxoid P30 epitope"
 FT Region 146..254
 FT /note= "109 C-terminal residues of human GDF-8"
 FT Misc-difference 90..91
 FT /note= "optionally replaced by Glu-Gly"
 FT Misc-difference 235..236
 FT /note= "optionally replaced by Glu-Gly"
 PN W0200105820-A2.
 XX
 XX 25-JAN-2001.
 XX
 XX 20-JUL-2000; 2000WO-DK00413.
 XX
 XX 20-JUL-1999; 99DK-0001014.
 XX 26-JUL-1999; 99US-0145275.
 XX
 XX (MEBI-) M & E BIOTECH AS.
 PA
 XX Halkier T, Mouritsen S, Klysner S;
 XX
 XX WPI: 2001-112680/12.
 DR
 PT Increasing the muscle mass of animals used in meat production by down
 PT regulating growth differentiation factor 8 (GDF-8) activity in the
 PT animal through induction of anti-GDF-8 antibody production -
 XX
 XX Example 1; Page 105-106; 110pp; English.
 PS
 CC The present sequence is that of AutoVac construct GDF-8 dimer
 CC comprising 2 copies of the 109-amino acid C-terminal region of human
 CC growth differentiation factor 8 (GDF-8, see AAF20141) covalently
 CC connected through the P2 and P30 T-cell epitopes (see AAB20143-44)
 CC of tctanus toxin. It is an object of the invention to produce a
 CC recombinant therapeutic vaccine that is capable of effecting
 CC down-regulation of GDF-8 in order to increase the muscle growth
 CC rate of farm animals. The vaccines (see AAB20145-53) are capable
 CC of breaking autotolerance against autologous GDF-8. They comprise
 CC the C-terminal portion of human GDF-8 in which a portion of the
 CC native sequence is replaced by a T-cell epitope such as P30, with
 CC minimal disturbance of the authentic 3-dimensional structure of
 CC the protein. Nucleic acids encoding the GDF-8 variants can be used
 CC for genetic immunisation of the animals. Down-regulation of GDF-8
 CC activity can increase muscle mass by up to at least 45% in cattle,
 CC pigs and poultry used for meat production, reducing the need for
 CC antibiotic feed additives. Anti-GDF8 vaccines can be used to
 CC treat human diseases such as cancer cachexia where muscle atrophy is
 CC pronounced and for patients suffering from acute and chronic heart
 CC failure.
 CC
 XX Sequence 254 AA;
 SO

0y	61	VH0ANPRGSAGPCCPPTLMSPIINMLYFNFGKE0IITGK1IPAMVVDRCGS	109
Db	61	vhdanprgsagpcpcptlmspimllyfngkeq1lygk1ipamvvdrcgs	109
RESULT 10			
ID	AAB20132	standard; Protein: 362 AA.	
XX	AAB20132		
AC	AAB20132:		
XX			
DT	30-APR-2001	(first entry)	
XX			
DE	Turkey growth differentiation factor 8.		
XX			
KW	Growth differentiation factor 8; GDF-8; myostatin; down-regulation;		
KW	vaccine; muscle; meat; cachexia; cardiomyopathy; turkey.		
XX			
OS	Meleagris gallopavo.		
XX			
PN	WO200105820-A2.		
PD			
XX	25-JAN-2001.		
XX			
PF	20-JUL-2000; 2000WO-DK00413.		
XX			
PR	20-JUL-1999; 99DK-0001014.		
PR	26-JUL-1999; 99US-0145275.		
PA	(MEB1-) M & E BIOTECH AS.		
XX			
PI	Halkier T, Mouritsen S, Klyener S;		
XX			
DR	WPI: 2001-112680/12.		
PT			
PT	Increasing the muscle mass of animals used in meat production by down		
PT	regulating growth differentiation factor 8 (GDF-8) activity in the		
PT	animal through induction of anti-GDF-8 antibody production		
XX			
PS	Example 1: Page 76-78; 110pp; English.		
XX			
CC	The present sequence is that of turkey growth differentiation factor		
CC	8 (GDF-8), also called myostatin. It is an object of the invention		
CC	to produce a recombinant therapeutic vaccine capable of effecting		
CC	down-regulation of GDF-8 in order to increase the muscle growth		
CC	rate of farm animals. Variants of GDF-8 (see AAB20145-53) are		
CC	provided that are capable of breaking autotolerance against		
CC	autologous GDF-8. These comprise a C-terminal portion of human		
CC	GDF-8 in which a portion of the native sequence is replaced by a		
CC	T-cell epitope such as the promiscuous tetanus toxin T-cell epitope		
CC	P2 or P30. Nucleic acids encoding the GDF-8 variants can be used		
CC	for genetic immunisation of the animals. Down-regulation of GDF-8		
CC	activity is used to increase muscle mass by up to at least 45%		
CC	in cattle, pigs and poultry used for meat production, reducing the		
CC	need for antibiotic feed-additives. Anti-GDF8 vaccines can be used		
CC	to treat human diseases such as cancer cachexia where muscle atrophy		
CC	is pronounced and for patients suffering from acute and chronic		
CC	heart failure.		
XX			
SO	Sequence 362 AA;		
Query Match	99.0%;	Score 622;	DB 22; Length 362;
Best Local Similarity	99.1%;	Pred. No. 4.9e-59;	
Matches 108; Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
0y	1	DFGLDCDEHSTESRCRCPLTVDFEAFGDMWLIAPRRYKANYCSGCECFVFLQKYPHRL	60
Db	254	dflgdcdeshstescrcrpltvdfefafgdmwliaprrykanycsgcecfvflqkyphtl	313
0y	61	VH0ANPRGSAGPCCPPTLMSPIINMLYFNFGKE0IITGK1IPAMVVDRCGS	109

Db 314 vhaqanprgsagpccptpkmsplmlyfngkeqilfygkipamvvdrcgcs 362

RESULT 11

AA63160

ID AAR63160 standard; Protein: 375 AA.

XX

XX AAR63160;

XX

XX 23-JUN-1995 (first entry)

XX

XX Human growth differentiation factor-8 protein.

XX

XX Growth differentiation factor-8; GDF-8; cell proliferation;

XX

XX adipocyte; obesity; transforming growth factor-beta.

XX

XX Homo sapiens.

XX

XX WO9421681-A.

XX

XX 29-SEP-1994.

XX

XX 18-MAR-1994; 94WO-US03019.

XX

XX 19-MAR-1993; 93US-0033923.

XX

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.

XX

XX Lee S, McPherron AC;

XX

XX WPI; 1994-316943/39.

XX

XX Q-PSDB; Q76372.

XX

XX New growth differentiation factor 8 - useful for treatment and

XX

XX diagnosis of cell proliferative disorders esp. of muscle.

XX

XX Claim 3; Page 58; 84pp: English.

XX

XX GDF-8 can be used to maintain cells before transplantation; to

XX

XX improve efficiency of cell fusion and to treat obesity or diseases

XX

XX related to abnormal adipocyte proliferation.

XX

XX Sequence 375 AA:

SQ

Query Match 99.0%; Score 622; DB 15; Length 375;

Best Local Similarity 99.1%; Pred. No. 5.1e-59;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYSCEGEFVFLQKYPHTL 60

Db 267 dfgldcdhstescrcrypltvdfefagwiiapkrkykanysgcegefvlqkyphtl 326

QY 61 VHOANPRGSGPCCPTPLMSPLMILYFNGKEQIIYKIPAMVVDRCGCS 109

Db 327 vhaqanprgsagpccptpkmsplmlyfngkeqilfygkipamvvdrcgcs 375

RESULT 12

AA69888

ID AAM69888 standard; Protein: 375 AA.

XX

XX AAM69888;

XX

XX 07-DEC-1998 (first entry)

XX

XX Chicken growth differentiation factor-8.

XX

XX Growth differentiation factor-8; GDF-8; chicken; transgenic animal;

XX

XX transforming growth factor-beta; muscle; meat; inhibitor; obesity;

XX

XX neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;

XX

XX therapy.

OS Gallus sp.

XX

XX Key

XX

XX Cleavage-site 263..266

XX

XX Protein 267..375

XX

XX /label= Mat_protein

XX

XX WO9833887-A1.

XX

XX 06-AUG-1998.

XX

XX 05-FEB-1998; 98WO-US02479.

XX

XX 23-MAY-1997; 97US-0862445.

XX

XX 05-FEB-1997; 97US-0795071.

XX

XX 28-APR-1997; 97US-0847910.

XX

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX

XX Lee S, McPherron AC;

XX

XX WPI; 1998-437444/37.

XX

XX N-PSDB; AAV45819.

XX

XX Transgenic animals with gene for growth differentiation factor-8

XX

XX disrupted - have increased muscle and reduced cholesterol contents,

XX

XX also use of GDF-8 inhibitors for treating cancer, obesity,

XX

XX neuromuscular disease

XX

XX Example 9; Fig 14c; 125pp; English.

XX

XX This is the amino acid sequence of chicken growth differentiation

XX

XX factor-8 (GDF-8), a novel member of the transforming growth factor-

XX

XX beta superfamily that appears to relate to various cell

XX

XX proliferative disorders, especially those involving muscle, nerve

XX

XX and adipose tissue. The sequence was deduced from a cDNA clone

XX

XX (see AAV45819) isolated from a skeletal muscle cDNA library. The

XX

XX invention provides novel mammalian and avian GDF-8 proteins (see

XX

XX AAM69883-92). A transgenic non-human animal is claimed in which

XX

XX GDF-8 expression is disrupted or interfered with. Also claimed

XX

XX are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb

XX

XX from these animals; (2) method for increasing muscle mass in

XX

XX animals by administering an antibody (Ab) that binds to GDF-8; (3)

XX

XX inhibiting the action of GDF-8 by treating foetal or adult muscle

XX

XX or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic

XX

XX acid encoding a GDF-8 protein truncated by loss of the C-terminal

XX

XX active fragment. The transgenic animals have increased muscle mass

XX

XX and for poultry reduced cholesterol contents. Method (3) is used

XX

XX to treat muscle wasting or neuromuscular diseases, muscular atrophy

XX

XX and aging, particularly muscular dystrophy, spinal cord or

XX

XX traumatic injuries, congestive or obstructive lung disease, AIDS

XX

XX and cachexia. Method (4) is used to treat cancer of muscle, GDF-8

XX

XX can be used to maintain myoblasts intended for transplanting or to

XX

XX improve efficiency of fusion. Ab can be used to detect and

XX

XX quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),

XX

XX also for immunotherapy and in vivo imaging.

XX

XX Sequence 375 AA:

SQ

Query Match 99.0%; Score 622; DB 19; Length 375;

Best Local Similarity 99.1%; Pred. No. 5.1e-59;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYSCEGEFVFLQKYPHTL 60

Db 267 dfgldcdhstescrcrypltvdfefagwiiapkrkykanysgcegefvlqkyphtl 326

QY 61 VHOANPRGSGPCCPTPLMSPLMILYFNGKEQIIYKIPAMVVDRCGCS 109

Db 327 vhaqanprgsagpccptpkmsplmlyfngkeqilfygkipamvvdrcgcs 375

RESULT 13
 AAW69891
 ID AAW69891 standard; Protein; 375 AA.
 AC AAW69891;
 DT 07-DEC-1998 (first entry)
 XX
 DE Pig growth differentiation factor-8.
 XX
 KW Growth differentiation factor-8; GDF-8; pig; transgenic animal;
 KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
 KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
 KW therapy.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 263..266
 FT Protein 267..375
 FT /label= Mat_protein
 XX
 MO9833887-A1.
 PD 06-AUG-1998.
 XX
 PF 05-FEB-1998; 98WO-US02479.
 XX
 PR 23-MAY-1997; 97US-0862445.
 PR 05-FEB-1997; 97US-0795071.
 PR 28-APR-1997; 97US-0847910.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Lee S, McPherron AC;
 XX
 DR WPI: 1998-437444/37.
 DR N-PSDB: AAW45822.
 XX
 PT Transgenic animals with gene for growth differentiation factor-8
 PT disrupted - have increased muscle and reduced cholesterol contents,
 PT also use of GDF-8 inhibitors for treating cancer, obesity,
 PT neuromuscular disease
 XX
 PS Example 9; Fig 14f; 125pp; English.
 XX
 CC This is the amino acid sequence of porcine growth differentiation
 CC factor-8 (GDF-8), a novel member of the transforming growth factor-
 CC beta superfamily that appears to relate to various cell
 CC proliferative disorders, especially those involving muscle, nerve
 CC and adipose tissue. The sequence was deduced from a cDNA clone
 CC (see AAW45822) isolated from a skeletal muscle cDNA library. The
 CC invention provides novel mammalian and avian GDF-8 proteins (see
 CC AAW69883-92). A transgenic non-human animal is claimed in which
 CC GDF-8 expression is disrupted or interfered with. Also claimed
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
 CC from these animals; (2) method for increasing muscle mass in
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
 CC active fragment. The transgenic animals have increased muscle mass
 CC and for poultry reduced cholesterol contents. Method (3) is used
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
 CC and aging, particularly muscular dystrophy, spinal cord or
 CC traumatic injuries, congestive or obstructive lung disease, AIDS
 CC and cachexia. Method (4) is used to treat cancer of muscle,
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
 CC can be used to maintain myoblasts intended for transplanting or to
 CC improve efficiency of fusion. Ab can be used to detect and
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
 CC also for immunotherapy and in vivo imaging.

XX
 SQ Sequence 375 AA:
 Query Match 99.0%; Score 622; DB 19; Length 375;
 Best Local Similarity 99.1%; Pred. No. 5.1e-59;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFGLCDDEHSTESRCRCRYPLVDFEAFGMDWIAPKRYKANYCSGECEFFLQKYPHTL 60
 DB 267 dfgldcdeshstescrcryplvdfefgmdwiiapkrkykanycsgecefflqkyphtl 326
 QY 61 VHQANPRGSAGPCCPPTLMSPINMLTFNGKEDITTKIPAMVYDRGCS 109
 DB 327 vhnqanprgsagpcctptlmspinmlyfngkeditlygkipamvdyrgcs 375
 RESULT 14
 AAW69885
 ID AAW69885 standard; Protein; 375 AA.
 AC AAW69885;
 DT 07-DEC-1998 (first entry)
 XX
 DE Human growth differentiation factor-8.
 XX
 KW Growth differentiation factor-8; GDF-8; human; transgenic animal;
 KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
 KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 71..73
 FT /note="Asn is N-glycosylated"
 FT Cleavage-site 263..266
 FT Protein 267..375
 FT /label= Mat_protein
 XX
 PN MO9833887-A1.
 PD 06-AUG-1998.
 XX
 PF 05-FEB-1998; 98WO-US02479.
 XX
 PR 23-MAY-1997; 97US-0862445.
 PR 05-FEB-1997; 97US-0795071.
 PR 28-APR-1997; 97US-0847910.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Lee S, McPherron AC;
 XX
 DR WPI: 1998-437444/37.
 DR N-PSDB: AAW45813.
 XX
 PT Transgenic animals with gene for growth differentiation factor-8
 PT disrupted - have increased muscle and reduced cholesterol contents,
 PT also use of GDF-8 inhibitors for treating cancer, obesity,
 PT neuromuscular disease
 XX
 PS Example 3; Fig 5c; 125pp; English.
 XX
 CC This is the amino acid sequence of human growth differentiation
 CC factor-8 (GDF-8), a novel member of the transforming growth factor-
 CC beta superfamily that appears to relate to various cell
 CC proliferative disorders, especially those involving muscle, nerve
 CC and adipose tissue. The sequence was deduced from a cDNA clone
 CC (see AAW45810) isolated from a skeletal muscle cDNA library. The
 CC invention provides novel mammalian and avian GDF-8 proteins (see
 CC AAW69883-92). A transgenic non-human animal is claimed in which

CC GDF-8 expression is disrupted or interfered with. Also claimed
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
 CC from these animals; (2) method for increasing muscle mass in
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
 CC active fragment. The transgenic animals have increased muscle mass
 CC and for poultry reduced cholesterol contents. Method (3) is used
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
 CC and aging, particularly muscular dystrophy, spinal cord or
 CC traumatic injuries, congestive or obstructive lung disease, AIDS
 CC and cachexia. Method (4) is used to treat cancer of muscle,
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
 CC can be used to maintain myoblasts intended for transplanting or to
 CC improve efficiency of fusion. Ab can be used to detect and
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
 CC also for immunotherapy and in vivo imaging.

Sequence 375 AA:

Query Match 99.0%; Score 622; DB 19; Length 375;
 Best Local Similarity 99.1%; Pred. No. 5.1e-59;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPRKRYKANYCSGCEPFLQKYPHTL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 267 dfgldcdenstescrcrypltvdfefgwdwliapkrkykanycsgecefliqkyphtl 326
 OY 61 VHOANPRGSAGPCCPTPLMSPIMLYFNKGKQIITYGKIPAMVVDRCGCS 109
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 327 vhoanprgsagpcpcptplmspimllyfnkgkqiygkipamvvdrcgcs 375

RESULT 15

AAW65460
 ID AAW65460 standard; Protein; 375 AA.

AC AAW65460;

DT 09-NOV-1998 (first entry)

DE Human growth differentiation factor-8.

DE Growth differentiation factor-8; GDF-8; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 71 /note="N-glycosylated"

FT Cleavage-site 263..266 /note="RXXR proteolytic cleavage site"

XX WO9835019-A1.

XX 13-AUG-1998.

XX 06-FEB-1998; 98WO-US02310.

XX 06-FEB-1997; 97US-0795671.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Lee S, McPherron AC, v

XX WPI; 1998-447217/38.

XX Transgenic animal growth differentiation factor-11 is inhibited - by
 PT insertion of transgene, also use of GDF-11 inhibitors for treating
 PT muscular wasting, neuromuscular disease, obesity
 XX

PS Example 3; Page 55-56; 89pp; English.

XX This is the amino acid sequence of human growth differentiation
 CC factor-8 (GDF-8). It shows a high degree of sequence homology
 CC to the newly identified human growth differentiation factor-11
 CC (GDF-11, see AAW65458). Alignment of the GDF-8 and GDF-11 sequences
 CC reveals potential N-linked glycosylation signals and putative
 CC proteolytic processing sites at analogous positions. The 2
 CC sequences are related not only in the C-terminal region following
 CC the putative cleavage site (90% amino acid sequence identity) but
 CC also in the pro-region of the molecules (45% amino acid sequence
 CC identity. Claimed transgenic animals in which GDF-11 production is
 CC reduced produce higher than normal levels of muscle and are useful
 CC in the food industry. GDF-11 polypeptides, polynucleotides and
 CC antibodies can be used to modulate GDF-11 activity or gene
 CC expression for treatment of cell proliferative disorders involving
 CC muscle, nerve and adipose tissue.

Sequence 375 AA:

Query Match 99.0%; Score 622; DB 19; Length 375;
 Best Local Similarity 99.1%; Pred. No. 5.1e-59;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPRKRYKANYCSGCEPFLQKYPHTL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 267 dfgldcdenstescrcrypltvdfefgwdwliapkrkykanycsgecefliqkyphtl 326
 OY 61 VHOANPRGSAGPCCPTPLMSPIMLYFNKGKQIITYGKIPAMVVDRCGCS 109
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 327 vhoanprgsagpcpcptplmspimllyfnkgkqiygkipamvvdrcgcs 375

Search completed: May 20, 2002, 09:21:47
 Job time: 82 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:20:25 ; Search time 13.12 Seconds
(Without alignments)
202.926 Million cell updates/sec

Title: US-09-754-826-2
Perfect score: 628
Sequence: 1 DFGLDCEHSTESRCRYPL.....KEQIITYKIPAMVDRCCS 109

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfilstl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	99.0	126	2	US-08-525-596B-6
2	622	99.0	126	3	US-09-177-860A-6
3	622	99.0	375	2	US-08-525-596B-14
4	622	99.0	375	2	US-08-765-875-5
5	622	99.0	375	3	US-08-795-671-5
6	622	99.0	375	3	US-09-177-860A-14
7	622	99.0	376	3	US-08-525-596B-12
8	622	99.0	376	3	US-09-177-860A-12
9	622	99.0	376	3	US-08-891-789B-6
10	611	97.3	375	3	US-08-891-789B-2
11	583	92.8	108	2	US-08-525-596B-8
12	583	92.8	108	3	US-09-177-860A-8
13	574	91.4	126	1	US-08-247-907A-2
14	574	91.4	126	1	US-08-452-772-2
15	574	91.4	126	1	US-08-765-875-4
16	574	91.4	126	3	US-08-795-671-4
17	574	91.4	126	4	US-09-414-234-2
18	574	91.4	126	5	PCT-US94-05288-2
19	574	91.4	362	1	US-08-247-907A-11
20	574	91.4	362	1	US-08-452-772-11
21	574	91.4	362	4	US-09-414-234-11
22	574	91.4	362	5	PCT-US94-05288-11
23	574	91.4	407	2	US-08-765-875-2
24	574	91.4	407	2	US-08-765-875-6
25	574	91.4	407	3	US-08-795-671-2
26	574	91.4	407	3	US-08-795-671-6
27	256	40.8	52	1	US-08-247-907A-4

28	256	40.8	52	1	US-08-452-772-4	Sequence 4, Appl1
29	256	40.8	52	4	US-09-414-234-4	Sequence 4, Appl1
30	256	40.8	52	5	PCT-US94-05288-4	Sequence 12, Appl1
31	241	38.4	128	1	US-08-455-550-12	Sequence 37, Appl1
32	235	37.4	115	1	US-08-197-792-37	Sequence 37, Appl1
33	235	37.4	115	1	US-08-459-850-37	Sequence 37, Appl1
34	235	37.4	115	1	US-08-459-850-37	Sequence 37, Appl1
35	235	37.4	120	1	US-08-481-377-22	Sequence 22, Appl1
36	235	37.4	120	2	US-08-491-835-20	Sequence 20, Appl1
37	235	37.4	120	3	US-09-153-733A-22	Sequence 22, Appl1
38	235	37.4	120	3	US-08-946-092A-20	Sequence 20, Appl1
39	235	37.4	120	4	US-09-172-062-20	Sequence 20, Appl1
40	235	37.4	120	4	US-08-624-635-20	Sequence 20, Appl1
41	235	37.4	120	5	PCT-US94-00666-22	Sequence 22, Appl1
42	235	37.4	120	5	PCT-US94-00666-22	Sequence 20, Appl1
43	235	37.4	121	1	US-08-581-529B-18	Sequence 18, Appl1
44	235	37.4	121	1	US-08-455-559-24	Sequence 24, Appl1
45	235	37.4	121	2	US-08-525-596B-28	Sequence 28, Appl1

ALIGNMENTS

RESULT 1
US-08-525-596B-6
Sequence 67, Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525, 596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-525-596B-6

Query Match 99.0%; Score 622; DB 2; Length 126;
Best Local Similarity 99.1%; Pred. No. 3.3e-66;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFGLDCEHSTESRCRYPLTVDFEAGMDWIIIPKRYKANVCSGCEFFVLRKYPHTL 60

Db 18 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 77
Qy 61 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 109
Db 78 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 126

RESULT 2
US-09-177-860A-6
Sequence 6, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-177-860A-6

Query Match 99.0%; Score 622; DB 3: Length 126;
Best Local Similarity 99.1%; Pred. No. 3.3e-66;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 60
Db 18 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 77
Qy 61 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 109
Db 78 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 126
RESULT 3
US-08-525-596B-14
Sequence 14, Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5099
TELEFAX: 619-678-5070
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-525-596B-14

Query Match 99.0%; Score 622; DB 2: Length 375;
Best Local Similarity 99.1%; Pred. No. 1.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 60
Db 267 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 326
Qy 61 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 109
Db 327 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 375
RESULT 4
US-08-765-875-5
Sequence 5, Application US/08765875
Patent No. 5914234
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERSON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,875
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,938
FILING DATE:
APPLICATION NUMBER: US/08/272,763
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3641
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-765-875-5

Query Match 99.0%; Score 622; DB 2; Length 375;
Best Local Similarity 99.1%; Pred. No. 1.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCEHSTESRCRYPPLVDFEARGWMIAPKRYKANYCGECEVFVLOKYPHTL 60
DB 267 DFGIDCEHSTESRCRYPPLVDFEARGWMIAPKRYKANYCGECEVFVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGKQIITGKIPANVVDRCGS 109
DB 327 VHOANPRGSAGPCCPTPLMSPINMLYFNKGKQIITGKIPANVVDRCGS 375

RESULT 5
US-08-795-671-5
Sequence 5, Application US/08795671
Patent No. 6008434
GENERAL INFORMATION:
APPLICANT: Se-Jin Lee and Alexandra McPherron
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HATLE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-795-671-5

Query Match 99.0%; Score 622; DB 3; Length 375;
Best Local Similarity 99.1%; Pred. No. 1.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCEHSTESRCRYPPLVDFEARGWMIAPKRYKANYCGECEVFVLOKYPHTL 60
DB 267 DFGIDCEHSTESRCRYPPLVDFEARGWMIAPKRYKANYCGECEVFVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGKQIITGKIPANVVDRCGS 109
DB 327 VHOANPRGSAGPCCPTPLMSPINMLYFNKGKQIITGKIPANVVDRCGS 375

RESULT 6
US-09-177-860A-14
Sequence 14, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hatle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-09-177-860A-14

Query Match 99.0%; Score 622; DB 3; Length 375;
Best Local Similarity 99.1%; Pred. No. 1.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTSRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 60
Db 267 DFGDDEHSTSRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 326
Qy 61 VHQANPRGSAGPCCTPTLSPINMLYFNKGEOIYYKIPAMVYDRGCS 109
Db 327 VHQANPRGSAGPCCTPTLSPINMLYFNKGEOIYYKIPAMVYDRGCS 375

RESULT 7
US-08-525-596B-12

; Sequence 12, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-525-596B-12

Query Match 99.0%; Score 622; DB 2; Length 376;
Best Local Similarity 99.1%; Pred. No. 1.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTSRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 60
Db 268 DFGDDEHSTSRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 327
Qy 61 VHQANPRGSAGPCCTPTLSPINMLYFNKGEOIYYKIPAMVYDRGCS 109
Db 328 VHQANPRGSAGPCCTPTLSPINMLYFNKGEOIYYKIPAMVYDRGCS 376

RESULT 8

US-09-177-860A-12
; Sequence 12, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/177,860A
; FILING DATE: 23-OCT-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/075003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-677-1456
; TELEFAX: 858-677-1465
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-177-860A-12

Query Match 99.0%; Score 622; DB 3; Length 376;
Best Local Similarity 99.1%; Pred. No. 1.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTSRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 60
Db 268 DFGDDEHSTSRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 327
Qy 61 VHQANPRGSAGPCCTPTLSPINMLYFNKGEOIYYKIPAMVYDRGCS 109
Db 328 VHQANPRGSAGPCCTPTLSPINMLYFNKGEOIYYKIPAMVYDRGCS 376

RESULT 9

US-08-891-789B-6
; Sequence 6, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobel, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:

4 MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,789B
FILING DATE: July 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 52836/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-891-789B-6

Query Match 99.0%; Score 622; DB 3; Length 376;
Best Local Similarity 99.1%; Pred. No. 1.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGSECFVLOKYPHTL 60
Db 268 DFGIDCDHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGSECFVLOKYPHTL 327
QY 61 VHQANPRGSAGPCTPTLMSPINMLYFNKGEOIYIKRIPAMVYDRCCGS 109
Db 328 VHQANPRGSAGPCTPTLMSPINMLYFNKGEOIYIKRIPAMVYDRCCGS 376

RESULT 10
US-08-891-789B-2
Sequence 2, Application US/08891789B
Patent No. 6103466
GENERAL INFORMATION:
APPLICANT: Grobet, Luc; Georges, Michel
TITLE OF INVENTION: Double-Muscling In Mammals
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
ZIP: M5L 1A9
COUNTRY: Canada
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER READABLE FORM:
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,789B
FILING DATE: July 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 52836/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-891-789B-2

Query Match 97.3%; Score 611; DB 3; Length 375;
Best Local Similarity 97.2%; Pred. No. 2.4e-64;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGSECFVLOKYPHTL 60
Db 267 DFGIDCDHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGSECFVLOKYPHTL 326
QY 61 VHQANPRGSAGPCTPTLMSPINMLYFNKGEOIYIKRIPAMVYDRCCGS 109
Db 327 VHQANPRGSAGPCTPTLMSPINMLYFNKGEOIYIKRIPAMVYDRCCGS 375

RESULT 11
US-08-525-596B-8
Sequence 8, Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION:

APPLICANT: Huyhn, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
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FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-525-596B-8

Query Match 92.8%; Score 583; DB 2; Length 108;
Best Local Similarity 99.0%; Pred. No. 1.1e-61;
Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGSECFVLOKYPHTL 60
Db 6 DFGIDCDHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGSECFVLOKYPHTL 65
QY 61 VHQANPRGSAGPCTPTLMSPINMLYFNKGEOIYIKRIPAMV 103
Db 66 VHQANPRGSAGPCTPTLMSPINMLYFNKGEOIYIKRIPAMV 108

